

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: SANOFI
- (B) STREET: 32,34 rue MARBEUF
- (C) CITY: PARIS
- (E) COUNTRY: FRANCE
- (F) POSTAL CODE (ZIP): 75374
- (G) TELEPHONE: 0153774000
- (H) TELEFAX: 0153774133

(ii) TITLE OF INVENTION: IL-13 receptor

(iii) NUMBER OF SEQUENCES: 4

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1539 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (F) TISSUE TYPE: Carcinoma
- (G) CELL TYPE: renal
- (H) CELL LINE: caki-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGTGCCTGTC	GGCGGGGAGA	GAGGCAATAT	CAAGGTTTA	AATCTGGAG	AAATGGCTTA	60
ATTICGTTGC	TTGGCTATCG	GATGCTTATA	TACCTTCTG	ATAAGCACAA	CATTTGGCTG	120
TACAAGCTTT	TGCACATTCAT	CTTCAGACAC	CGAGATAAAA	GTAAACCCTC	CTCAGGATTT	180
TGAGATAGTG	GATTATGAAG	AGAACCCGGA	TACTTAGGTT	ATCTCTATT	GCAATGGCAA	240
CCCCCACTGT	CTCTGGATCA	TTTTGTGTTG	TGAAAGGAAT	GCACAGTGGAA	ATATGAAC	300
AAATACCGAA	ACATTGGTAG	TGAAACATGG	AAGGCTAGTG	TAGAGGTTAC	CATCATTACT	360
AAGAATCTAC	ATTACAAAGA	TGGGTTTGAT	CTTAACAAGG	GCATTGAATT	ATAGAAGGGC	420
GAAGATACAC	ACGCTTTAC	CATGGCAATG	CACAAATGGA	TCAGAAGTTC	AAAGTTCCAA	480
TTGCTAGGAG	TGGGCAGAAA	CTACTTATTG	GATATCACCA	CAAGGAATT	CAGAAACTAA	540
AGTTCAAGGAT	TAAGTTTGG	GTAGAATGGA	TTGCGTATAT	TACAATTGGC	AATATTACT	600
CTGTTCTTGG	AAACCTGGCA	TAGGTTACAT	TATGTCTGGG	TACTTCTTGA	TACCAATTAC	660
AACTTGTGTTT	ACTGGTATGA	GGGCTTGGAT	CATGCATTAA	ATATATTGG	AAACAGTGTG	720
TTGATTACAT	CAAGGCTGAT	GGACAAAATA	TAGGATGCAG	ATTTCCTAT	TTGGCAATAA	780

AGGAGCAGTG AGGCATCAGA CTATAAAGAT TTCTATATT GTGTTAATGG ATCATCAGAG	840
AACAAGCTG AAATATCAAG GAATCAGATC CAGTTATTTC ACTTTTCAGC TTCAAAATAT	900
AGTTAACCT TTGCCGCCAG TCAGTTGGAA ATATCTTACT TTTACTCGGG AGAGTTCATG	960
TGAAATTAAG CTGAAATGGA GCATACCTTT GTTTAGGCCT GGACCTATTG CAGCAAGGTG	1020
TTTGATTAT GAAATTGAGA TCAGAGAAGA TGATACTACC GAAAGCATGG AGGAATTITG	1080
GTGACTGCTA CAGTTGAAAA TGAAACATAC ACCTTGAAAA CAACAAATGA AACCCGAATA	1140
ATAGAGTTT TAGTAGCAAT TATGCTTGT AGTAAGAACG AAAGTGAATA TTTATTGCTC	1200
AGATGACGGA ATTTGGCAA AGAATCAAGT AGTGAGTGG A GTGATAAAACA ATGCTGGAA	1260
GGTGAAGACC TATCGAAGAA AACTTGCTA GTAGCTGGG TCGTTTCTGG CTACCATTG	1320
GTTTCATCTT AATATTAGTT ATATTGTAA CCGGTCTGCT TAGTGAATGT TGCCTAAGCC	1380
AAACACCTAC CCAAAAATGA TTCCAGAATT TTTCTGTGAT ACATGAAGAA GATTTCATC	1440
TTTCCATATC AAGAGACATG GTATTGACTC AACAGTTCC AGTCATGGCC AAATGTTCAA	1500
TATGAGTCTC AATAAACTGA ATTTTTCTTG CGAATGTTG	1539

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens
(F) TISSUE TYPE: Carcinoma
(G) CELL TYPE: renal
(H) CELL LINE: Caki-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ala Phe Val Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile
1 5 10 15

Ser Thr Thr Phe Gly Cys Thr Ser Ser Ser Asp Thr Glu Ile Lys Val
 20 25 30

Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr
35 40 45

Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu
50 55 60

Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr
65 70 75 80

Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp
85 90 95

Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln
100 105 110

Cys Thr Asn Gly Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr
115 120 125

Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp
 130 135 140
 Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly
 145 150 155 160
 Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu
 165 170 175
 Gly Leu Asp His Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly
 180 185 190
 Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys
 195 200 205
 Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg
 210 215 220
 Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro
 225 230 235 240
 Pro Val Tyr Leu Thr Phe Thr Arg Glu Ser Ser Cys Glu Ile Lys Leu
 245 250 255
 Lys Trp Ser Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Asp Tyr
 260 265 270
 Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr Leu Val Thr Ala Thr Val
 275 280 285
 Glu Asn Glu Thr Tyr Thr Leu Lys Thr Thr Asn Glu Thr Arg Gln Leu
 290 295 300
 Cys Phe Val Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly
 305 310 315 320
 Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys Trp Glu Gly Glu Asp Leu
 325 330 335
 Ser Lys Lys Thr Leu Leu Arg Phe Trp Leu Pro Phe Gly Phe Ile Leu
 340 345 350
 Ile Leu Val Ile Phe Val Thr Gly Leu Leu Leu Arg Lys Pro Asn Thr
 355 360 365
 Tyr Pro Lys Met Ile Pro Glu Phe Phe Cys Asp Thr
 370 375 380

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4009 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (F) TISSUE TYPE: Carcinoma
 - (G) CELL TYPE: RENAL
 - (H) CELL LINE: Caki-1

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TCAGCCCGGC CGGGCTCCGA GGCGAGAGGC TGCATGGAGT GGCCGGCGCG GCTCTGCGGG	60
CTGTGGCGC TGCTGCTCTG CGCCGGCGGC GGGGGCGGGG GCGGGGGCGC CGCGCCTACG	120
GAAACTCAGC CACCTGTGAC AAATTGAGT GTCTCTGTTG AAAACCTCTG CACAGTAATA	180
TGGACATGGA ATCCACCCGA GGGAGCCAGC TCAAATTGTA GTCTATGGTA TTTTAGTCAT	240
TTTGGCGACA AACAAAGATAA GAAAATAGCT CCGGAAACTC GTCGTTCAAT AGAAAGTACCC	300
CTGAATGAGA GGATTTGTCT GCAAGTGGGG TCCCAGTGTG GCACCAATGA GAGTGAGAAG	360
CCTAGCATTT TGTTGAAAA ATGCATCTCA CCCCCAGAAG GTGATCCTGA GTCTGCTGTG	420
ACTGAGCTTC AATGCATTG GCACAACCTG AGCTACATGA AGTGTCTTG GCTCCCTGGA	480
AGGAATACCA GTCCCGACAC TAACTATACT CTCTACTATT GGCACAGAAG CCTGGAAAAA	540
ATTCAATCAAT GTGAAAACAT CTTTAGAGAA GGCCAATACT TTGGTTGTTG CTTTGATCTG	600
ACCAAAGTGA AGGATTCCAG TTTGAACAA CACAGTGTCC AAATAATGGT CAAGGATAAT	660
GCAGGAAAAA TTAAACCATC CTTCAATATA GTGCCTTAA CTTCCCGTGT GAAACCTGAT	720
CCTCCACATA TTAAAAACCT CTCCTTCCAC AATGATGACC TATATGTGCA ATGGGAGAAT	780
CCACAGAATT TTATTAGCAG ATGCCATTG TATGAAGTAG AAGTCATAA CAGCCAAACT	840
GAGACACATA ATGTTTCTA CGTCCAAGAG GCTAAATGTG AGAATCCAGA ATTTGAGAGA	900
AATGTGGAGA ATACATCTTGT TTTCATGGTC CCTGGTGTTC TTCCTGATAC TTTGAACACA	960
GTCAGAATAA GAGTCAAAAC AAATAAGTTA TGCTATGAGG ATGACAAACT CTGGAGTAAT	1020
TGGAGCCAAG AAATGAGTAT AGGTAAGAAG CGCAATTCCA CACTCTACAT AACCATGTTA	1080
CTCATTGTTG CAGTCATCGT CGCAGGTGCA ATCATAGTAC TCCTGCTTTA CCTAAAAAGG	1140
CTCAAGATTA TTATATTCCC TCCAATTCCCT GATCCTGGCA AGATTTTAA AGAAATGTTT	1200
GGAGACCAGA ATGATGATAC TCTGCACTGG AAGAAGTAGC ACATCTATGA GAAGCAAACC	1260
AAGGAGGAAA CCGACTCTGT AGTGCTGATA GAAAACCTGA AGAAAGCCTC TCAGTGATGG	1320
AGATAATTAA TTTTTACCTT CACTGTGACC TTGAGAAGAT TCTTCCCATT CTCCATTGTT	1380
TATCTGGAA CTTATTAAAT GGAAACTGAA ACTACTGCAC CATTAAAAA CAGGCAGCTC	1440
ATAAGAGCCA CAGGTCTTTA TGTTGAGTCG CGCACCGAAA AACTAAAAAT AATGGCGCT	1500
TTGGAGAAGA GTGTGGAGTC ATTCTCATTG AATTATAAAA GCCAGCAGGC TTCAAACACT	1560
GGGACAAAGC AAAAAGTGAT GATAGTGGTG GAGTTAAC TATCAAGAGT TGTGACAAC	1620
TCCTGAGGGA TCTATACCTG CTTTGTGTTC TTTGTGTCAA CATGAACAAA TTTTATTGTT	1680
AGGGGAACTC ATTTGGGGTG CAAATGCTAA TGTCAAACCTT GAGTCACAAA GAACATGTAG	1740
AAAACAAAAT GGATAAAAATC TGATATGTAT TGTGAGGAT CCTATTGAAC CATGTTGTTG	1800
GCTATTAAAA CTCTTTAAC AGTCTGGCT GGGTCCGGTG GCTCACGCCT GTAATCCCAG	1860
CAATTGGGA GTCCGAGGCG GGCAGGATCAC TCGAGGTCAG GAGTTCCAGA CCAGCCTGAC	1920
CAAAATGGTG AACCTCCTC TCTACTAAAA CTACAAAAAT TAACTGGGTG TGGTGGCGCG	1980
TGCCTGTAAT CCCAGCTACT CGGGAAGCTG AGGCAGGTGA ATTGTTGAA CCTGGGAGGT	2040

GGAGGTTGCA	GTGAGCAGAG	ATCACACCCAC	TGCACCTCTAG	CCTGGGTGAC	AGAGCAAGAC	2100
TCTGTCTAAA	AAACAAAACA	AAACAAAACA	AAACAAAAAA	ACCTCTTAAT	ATTCTGGAGT	2160
CATCATTCCC	TTCGACAGCA	TTTCCTCTG	CTTGAAAGC	CCCAGAAATC	AGTGTGGCC	2220
ATGATGACAA	CTACAGAAAA	ACCAGAGGCA	GCTTCTTGC	CAAGACCTTT	CAAAGCCATT	2280
TTAGGCTGTT	AGGGGCAGTG	GAGGTAGAAT	GAETCCTTGG	GTATTAGAGT	TTCAACCATG	2340
AAGTCTCTAA	CAATGTATTT	TCTTCACCTC	TGCTACTCAA	GTAGCATTAA	CTGTGTCTTT	2400
GGTTTGTGCT	AGGCCCGGG	GTGTGAAGCA	CAGACCCCTT	CCAGGGTTT	ACAGTCTATT	2460
TGAGACTCCT	CAGTTCTTGC	CACTTTTTT	TTAATCTCC	ACCAGTCATT	TTTCAGACCT	2520
TTTAACTCCT	CAATTCCAAC	ACTGATTCC	CCTTTGCAT	TCTCCCTCCT	TCCCTTCCTT	2580
GTAGCCTTTT	GACTTTCATT	GGAAATTAGG	ATGTAATCT	GCTCAGGAGA	CCTGGAGGAG	2640
CAGAGGATAA	TTAGCATCTC	AGGTTAACGTG	TGAGTAATCT	GAGAAACAAT	GACTAATTCT	2700
TGCATATTTT	GTAACTTCCA	TGTGAGGTT	TTCAGCATTG	ATATTTGTCC	ATTTTCTAAA	2760
CAGAGATGAG	GTGGTATCTT	CACGTAGAAC	ATTGGTATTG	GCTTGAGAAA	AAAAGAATAG	2820
TTGAACCTAT	TTCTCTTCT	TTACAAGATG	GGTCCAGGAT	TCCTCTTTTC	TCTGCCATAA	2880
ATGATTAATT	AAATAGCTTT	TGTGTCTTAC	ATTGGTAGCC	AGCCAGCCAA	GGCTCTGTTT	2940
ATGCTTTGG	GGGGCATATA	TTGGGTTCCA	TTCTCACCTA	TCCACACAAAC	ATATCCGTAT	3000
ATATCCCTC	TACTCTTACT	TCCCCAAAT	TTAAAGAAGT	ATGGAAATG	AGAGGCATT	3060
CCCCCACCCC	ATTTCTCTCC	TCACACACAG	ACTCATATTA	CTGGTAGGAA	CTTGAGAACT	3120
TTATTTCCAA	GTTGTTCAA	CATTACCAA	TCATATTAAT	ACAATGATGC	TATTTGCAAT	3180
TCCTGCTCCT	AGGGGAGGGG	AGATAAGAAA	CCCTCACTCT	CTACAGGTTT	GGGTACAAGT	3240
GGCAACCTGC	TTCCATGGCC	GTGTAGAAC	ATGGTGCCT	GGCTTCTCTG	AGGAAGCTGG	3300
GGTTCATGAC	AATGGCAGAT	GTAAAGTTAT	TCTTGAAGTC	AGATTGAGGC	TGGGAGACAG	3360
CCGTAGTAGA	TGTTCTACTT	TGTTCTGCTG	TTCTCTAGAA	AGAATATTTG	GTTCCTGT	3420
ATAGGAATGA	GATTAATTCC	TTTCAGGTA	TTTTATAATT	CTGGGAAGCA	AAACCCATGC	3480
CTCCCCCTAG	CCATTTTAC	TGTTATCCTA	TTTAGATGGC	CATGAAGAGG	ATGCTGTGAA	3540
ATTCCCAACA	AACATTGATG	CTGACAGTC	TGCAGTCTGG	GAGTGGGAA	GTGATCTTT	3600
GTTCCCATCC	TCTTCTTTTA	GCAGTAAAT	AGCTGAGGGA	AAAGGGAGGG	AAAAGGAAGT	3660
TATGGGAATA	CCTGTGGTGG	TTGTGATCCC	TAGGTCTTGG	GAGCTCTGG	AGGTGTCTGT	3720
ATCAGTGGAT	TTCCCATCCC	CTGTGGAAA	TTAGTAGGCT	CATTTACTGT	TTTAGGTCTA	3780
GCCTATGTGG	ATTTTTCTCCT	AACATACCTA	AGCAAACCC	GTGTCAGGAT	GGTAATTCTT	3840
ATTCTTCGT	TCAGTTAACGT	TTTCCCTTC	ATCTGGGCAC	TGAAGGGATA	TGTGAAACAA	3900
TGTTAACATT	TTTGGTAGTC	TTCAACCAGG	GATTGTTCT	GTTAACCTTC	TTATAGGAAA	3960
GCTTGAGTAA	AATAAAATATT	GTCTTTTGT	ATGTCACCCA	AAAAAAA		4009

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

DRAFT - DO NOT CITE

- (A) LENGTH: 427 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens
(F) TISSUE TYPE: Carcinoma
(G) CELL TYPE: renal
(H) CELL LINE: Caki-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Glu Trp Pro Ala Arg Leu Cys Gly Leu Trp Ala Leu Leu Cys
 1 . 5 10 15
 Ala Gly Gly Gly Gly Gly Gly Ala Ala Pro Thr Glu Thr Gln
 20 25 30
 Pro Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val
 35 40 45
 Ile Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu
 50 55 60
 Trp Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro
 65 70 75 80
 Glu Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu
 85 90 95
 Gln Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile
 100 105 110
 Leu Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala
 115 120 125
 Val Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys
 130 135 140
 Ser Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu
 145 150 155 160
 Tyr Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile
 165 170 175
 Phe Arg Glu Gly Gln Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val
 180 185 190
 Lys Asp Ser Ser Phe Glu Gln His Ser Val Gln Ile Met Val Lys Asp
 195 200 205
 Asn Ala Gly Lys Ile Lys Pro Ser Phe Asn Ile Val Pro Leu Thr Ser
 210 215 220
 Arg Val Lys Pro Asp Pro Pro His Ile Lys Asn Leu Ser Phe His Asn
 225 230 235 240
 Asp Asp Leu Tyr Val Gln Trp Glu Asn Pro Gln Asn Phe Ile Ser Arg
 245 250 255
 Cys Leu Phe Tyr Glu Val Glu Val Asn Asn Ser Gln Thr Glu Thr His
 260 265 270
 Asn Val Phe Tyr Val Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu
 275 280 285

Arg Asn Val Glu Asn Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro
290 295 300

Asp Thr Leu Asn Thr Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys
305 310 315 320

Tyr Glu Asp Asp Lys Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile
325 330 335

Gly Lys Lys Arg Asn Ser Thr Leu Tyr Ile Thr Met Leu Leu Ile Val
340 345 350

Pro Val Ile Val Ala Gly Ala Ile Ile Val Leu Leu Tyr Leu Lys
355 360 365

Arg Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile
370 375 380

Phe Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys
385 390 395 400

Lys Tyr Asp Ile Tyr Glu Lys Gln Thr Lys Glu Glu Thr Asp Ser Val
405 410 415

Val Leu Ile Glu Asn Leu Lys Lys Ala Ser Gln
420 425

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